

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 01:38:39 ; Search time 35297.7 Seconds
 (without alignments)
 17607.528 Million cell updates/sec

Title: US-10-757-343-2
 Perfect score: 9719
 Sequence: 1 tggaagggctaattcactcc.....gtggaaaatctctagcaggt 9719

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*
 1: gb_env:*
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 3: gb_ph:*
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 5: gb_pr:*
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 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	9531.2	98.1	9719	2	AR268768	AR268768 Sequence
2	9531.2	98.1	9719	10	HIVHXB2CG	K03455 Human immun

3	9513.6	97.9	9770	10	HIVPV22	K02083 Human immun
4	9511.6	97.9	9749	2	I07983	I07983 Sequence 1
5	9507	97.8	9748	10	REHTLV3	X01762 Human T-cel
6	9499	97.7	9748	2	E01099	E01099 DNA sequenc
7	9487	97.6	9752	10	HIVMCK1	D86068 Human immun
8	9478.6	97.5	9754	10	HIV2132	D86069 Human immun
9	9433.8	97.1	9609	2	AR607371	AR607371 Sequence
10	9433.8	97.1	9609	10	HIV1U12055	U12055 Human immun
11	9385.6	96.6	9795	10	HIVTH475A	L31963 Human immun
12	9208.4	94.7	14824	8	AF324493	AF324493 HIV-1 vec
13	9206.8	94.7	9709	2	AR067813	AR067813 Sequence
14	9206.8	94.7	9709	2	BD238372	BD238372 Virus vac
15	9206.8	94.7	9709	2	AR224437	AR224437 Sequence
16	9206.8	94.7	9709	2	AR352469	AR352469 Sequence
17	9206.8	94.7	9709	2	AX032749	AX032749 Sequence
18	9206.8	94.7	9709	10	HIVNL43	M19921 Human immun
19	9109	93.7	9781	10	HIVF12CG	Z11530 Human Immun
20	9084	93.5	9699	10	AF070521	AF070521 HIV-1 E9
21	9001.2	92.6	9181	2	AX074066	AX074066 Sequence
22	9001.2	92.6	9181	10	AF033819	AF033819 HIV-1, co
23	8979.8	92.4	9193	2	A04321	A04321 Human immun
24	8975.4	92.3	9213	2	E00987	E00987 Genomic DNA
25	8970.6	92.3	9193	2	A07867	A07867 Human immun
26	8952.4	92.1	9213	2	I04549	I04549 Sequence 11
27	8940.8	92.0	9229	10	HIVBRUCG	K02013 Human immun
28	8928.2	91.9	9688	10	AY835754	AY835754 HIV-1 iso
29	8903.6	91.6	9697	10	AY835779	AY835779 HIV-1 iso
30	8900	91.6	9730	10	AY835770	AY835770 HIV-1 iso
31	8859	91.2	9688	10	AY835765	AY835765 HIV-1 iso
32	8836.8	90.9	9733	10	AY835771	AY835771 HIV-1 iso
33	8826.2	90.8	9703	10	AY835762	AY835762 HIV-1 iso
34	8823.6	90.8	9712	10	AY835781	AY835781 HIV-1 iso
35	8819.8	90.7	9703	10	AY835777	AY835777 HIV-1 iso
36	8814.8	90.7	9747	10	AY835759	AY835759 HIV-1 iso
37	8806.8	90.6	9715	10	AY835766	AY835766 HIV-1 iso
38	8793	90.5	9718	10	AY835749	AY835749 HIV-1 iso
39	8791.2	90.5	9700	10	AY835755	AY835755 HIV-1 iso
40	8788.4	90.4	9715	10	AF004394	AF004394 HIV-1 str
41	8782.8	90.4	9749	10	AY835760	AY835760 HIV-1 iso
42	8780.8	90.3	9739	10	AF042101	AF042101 HIV-1 iso
43	8774	90.3	9711	10	HIVYU10X	M93259 Human immun
44	8767.2	90.2	9739	10	AF003887	AF003887 HIV-1 chi
45	8763.8	90.2	9664	10	AY835780	AY835780 HIV-1 iso

ALIGNMENTS

RESULT 1

AR268768

LOCUS	AR268768	9719 bp	DNA	linear	PAT 10-APR-2003
DEFINITION	Sequence 1 from patent US 6500623.				
ACCESSION	AR268768				
VERSION	AR268768.1 GI:29699384				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				

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OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 15:50:12 ; Search time 347.96 Seconds
(without alignments)
16207.366 Million cell updates/sec

Title: US-10-757-343-3
Perfect score: 3014
Sequence: 1 ggcgggccgctctagactag.....ggatccgcggccgctctaga 3014

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Query	Match	Length	DB	ID		
No.	Score						
c 1	2759	91.5	5108	3	US-09-628-730-51		Sequence 51, Appl
c 2	2759	91.5	5108	3	US-09-628-730-52		Sequence 52, Appl
c 3	2759	91.5	5111	3	US-09-628-730-55		Sequence 55, Appl
c 4	2759	91.5	5185	3	US-09-628-730-47		Sequence 47, Appl
c 5	2759	91.5	5188	3	US-09-628-730-59		Sequence 59, Appl
c 6	2759	91.5	5254	3	US-09-628-730-60		Sequence 60, Appl
c 7	2754.2	91.4	5899	3	US-09-173-053-2		Sequence 2, Appli

c	8	2742.2	91.0	5845	3	US-09-173-053-1	Sequence 1, Appli
c	9	2665.2	88.4	6978	3	US-09-872-733A-15	Sequence 15, Appl
c	10	2665.2	88.4	8366	3	US-09-872-733A-6	Sequence 6, Appli
c	11	2662.2	88.3	5900	2	US-08-663-998-1	Sequence 1, Appli
c	12	2662.2	88.3	5952	2	US-08-663-998-2	Sequence 2, Appli
c	13	2660.6	88.3	5676	2	US-08-663-998-3	Sequence 3, Appli
c	14	2660.6	88.3	5682	2	US-08-663-998-4	Sequence 4, Appli
c	15	2427.6	80.5	15538	3	US-09-554-337-1	Sequence 1, Appli
c	16	2418.2	80.2	4864	3	US-09-340-798A-1	Sequence 1, Appli
c	17	2418.2	80.2	4864	4	US-09-393-803-14	Sequence 14, Appl
c	18	2418.2	80.2	7003	3	US-09-913-909-1	Sequence 1, Appli
c	19	2418.2	80.2	7073	3	US-09-913-909-2	Sequence 2, Appli
c	20	2418.2	80.2	7272	3	US-09-913-909-4	Sequence 4, Appli
c	21	2418.2	80.2	7285	3	US-09-913-909-3	Sequence 3, Appli
c	22	2416.6	80.2	4865	5	US-10-204-200-1	Sequence 1, Appli
c	23	2394.6	79.4	4915	3	US-09-173-053-7	Sequence 7, Appli
c	24	2149.4	71.3	5859	5	US-09-826-206A-3	Sequence 3, Appli
	25	1898.4	63.0	4646	3	US-09-485-286-14	Sequence 14, Appl
	26	1805.4	59.9	4296	2	US-08-316-950-15	Sequence 15, Appl
	27	1805.4	59.9	4296	7	PCT-US95-12642-15	Sequence 15, Appl
	28	1805.4	59.9	4352	2	US-08-316-950-16	Sequence 16, Appl
	29	1805.4	59.9	4352	7	PCT-US95-12642-16	Sequence 16, Appl
	30	1805.4	59.9	6047	2	US-08-316-950-12	Sequence 12, Appl
	31	1805.4	59.9	6047	7	PCT-US95-12642-12	Sequence 12, Appl
	32	1769.4	58.7	3993	2	US-08-316-950-14	Sequence 14, Appl
	33	1769.4	58.7	3993	7	PCT-US95-12642-14	Sequence 14, Appl
	34	1769.4	58.7	6044	2	US-08-316-950-18	Sequence 18, Appl
	35	1769.4	58.7	6044	7	PCT-US95-12642-18	Sequence 18, Appl
	36	1768.4	58.7	4120	2	US-07-977-630-20	Sequence 20, Appl
c	37	1768.4	58.7	4120	2	US-07-977-630-21	Sequence 21, Appl
	38	1768.4	58.7	4120	2	US-08-316-950-11	Sequence 11, Appl
	39	1768.4	58.7	4120	7	PCT-US95-12642-11	Sequence 11, Appl
	40	1768.4	58.7	4505	2	US-08-316-950-13	Sequence 13, Appl
	41	1768.4	58.7	4505	7	PCT-US95-12642-13	Sequence 13, Appl
	42	1768.4	58.7	6171	2	US-08-316-950-17	Sequence 17, Appl
	43	1768.4	58.7	6171	7	PCT-US95-12642-17	Sequence 17, Appl
c	44	1499.6	49.8	3987	3	US-09-082-649B-83	Sequence 83, Appl
c	45	1499.6	49.8	3987	3	US-09-965-101-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1

US-09-628-730-51/c

; Sequence 51, Application US/09628730

; Patent No. 6759393

; GENERAL INFORMATION:

; APPLICANT: Morsey, Mohamad

; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE

; TITLE OF INVENTION: COMPOSITIONS

; FILE REFERENCE: PC10525B

; CURRENT APPLICATION NUMBER: US/09/628,730

; CURRENT FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 51

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OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 02:58:50 ; Search time 27527.4 Seconds
(without alignments)
19743.258 Million cell updates/sec

Title: US-10-757-343-2
Perfect score: 9719
Sequence: 1 tggaagggttaattcactcc.....gtggaaaatctctagcaggt 9719

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: gb_est7:*
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10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query						Description
	No.	Score	Match	Length	DB	ID	
c	1	466	4.8	527	11	BH886550	BH886550 LB00861a.
	2	416.8	4.3	448	5	CK082452	CK082452 81286rsic
	3	416.8	4.3	462	5	CK084149	CK084149 77655rsic

	4	416.8	4.3	462	8	CO838386	CO838386 LM_GL5_00
	5	416.8	4.3	467	5	CK084626	CK084626 84293rsic
	6	414.8	4.3	443	5	CK084791	CK084791 84281rsic
	7	411.8	4.2	443	5	CK084400	CK084400 83872rsic
	8	411.8	4.2	448	5	CK077577	CK077577 79154rsic
c	9	411.2	4.2	839	14	DU665892	DU665892 Ciuffi-HI
	10	410.6	4.2	843	14	DU667159	DU667159 Ciuffi-HI
	11	410.6	4.2	852	14	DU665880	DU665880 Ciuffi-HI
	12	404.8	4.2	459	5	CK080759	CK080759 79881rsic
c	13	404.4	4.2	845	14	DU667190	DU667190 Ciuffi-HI
	14	399.8	4.1	445	5	CK083896	CK083896 85763rsic
	15	399.8	4.1	448	5	CK081454	CK081454 81192rsic
c	16	397.4	4.1	818	14	DU666770	DU666770 Ciuffi-HI
	17	395.8	4.1	432	5	CK078909	CK078909 84577rsic
	18	392.2	4.0	422	8	CO838387	CO838387 LM_GL5_00
	19	391.8	4.0	432	5	CK076236	CK076236 77446rsic
	20	390.8	4.0	419	5	CK076309	CK076309 79822rsic
	21	390.8	4.0	431	8	CV101630	CV101630 UMC-pcryb
	22	384.8	4.0	425	5	CK077626	CK077626 85348rsic
	23	382.8	3.9	423	5	CK081960	CK081960 84291rsic
c	24	356.2	3.7	364	14	DU638111	DU638111 Ciuffi-HI
c	25	301.2	3.1	342	8	CV101352	CV101352 UMC-pcryb
	26	297.8	3.1	348	5	CK080432	CK080432 84150rsic
c	27	297.2	3.1	317	1	AB036462	AB036462 AB036462
c	28	282.6	2.9	330	13	CL293849	CL293849 02S0349-0
	29	251.6	2.6	284	5	CK078901	CK078901 77490rsic
	30	171.2	1.8	199	5	CK084529	CK084529 86382rsic
c	31	169.2	1.7	592	14	DU637731	DU637731 Ciuffi-HI
c	32	163.2	1.7	835	14	DU666050	DU666050 Ciuffi-HI
	33	163.2	1.7	849	14	DU667286	DU667286 Ciuffi-HI
	34	145.8	1.5	1339	14	DU799820	DU799820 lv01_fp00
	35	139.4	1.4	1381	14	DU799984	DU799984 lv01_fp00
	36	138.8	1.4	1347	14	DU799995	DU799995 lv01_fp00
	37	137.6	1.4	1396	14	DU799626	DU799626 lv01_fp00
	38	137.4	1.4	1414	14	DU799673	DU799673 lv01_fp00
	39	137	1.4	1360	14	DU800625	DU800625 lv01_fp00
	40	136.4	1.4	1385	14	DU799681	DU799681 lv01_fp00
	41	136.2	1.4	1368	14	DU799697	DU799697 lv01_fp00
	42	135.6	1.4	1217	14	DU800092	DU800092 lv01_fp00
	43	135.6	1.4	1383	14	DU799713	DU799713 lv01_fp00
	44	135.2	1.4	1380	14	DU799993	DU799993 lv01_fp00
	45	135	1.4	1370	14	DU799677	DU799677 lv01_fp00

ALIGNMENTS

RESULT 1
BH886550/c
LOCUS BH886550 527 bp DNA linear GSS 07-AUG-2002
DEFINITION LB00861a.d_SP6.1 Leishmania major Friedlin BAC Library Leishmania major genomic clone LB00861a, genomic survey sequence.
ACCESSION BH886550
VERSION BH886550.1 GI:22130945
KEYWORDS GSS.
SOURCE Leishmania major
ORGANISM Leishmania major

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OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 01:38:39 ; Search time 10946.3 Seconds
(without alignments)
17607.528 Million cell updates/sec

Title: US-10-757-343-3
Perfect score: 3014
Sequence: 1 ggcgggccgctctagactag.....ggatccgcggccgctctaga 3014

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

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SUMMARIES

Result	No.	Score	% Match	Query Length	DB	ID	Description
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c	2	2759	91.5	5108	2	BD000698	BD000698 Growth ho

c	3	2759	91.5	5108	2	AR562804	AR562804	Sequence
c	4	2759	91.5	5108	2	AR562805	AR562805	Sequence
c	5	2759	91.5	5108	2	AX138932	AX138932	Sequence
c	6	2759	91.5	5108	2	AX138933	AX138933	Sequence
c	7	2759	91.5	5111	2	BD000701	BD000701	Growth ho
c	8	2759	91.5	5111	2	AR562808	AR562808	Sequence
c	9	2759	91.5	5111	2	AX138936	AX138936	Sequence
c	10	2759	91.5	5185	2	BD000693	BD000693	Growth ho
c	11	2759	91.5	5185	2	AR562800	AR562800	Sequence
c	12	2759	91.5	5185	2	AX138928	AX138928	Sequence
c	13	2759	91.5	5188	2	BD000705	BD000705	Growth ho
c	14	2759	91.5	5188	2	AR562812	AR562812	Sequence
c	15	2759	91.5	5188	2	AX138940	AX138940	Sequence
c	16	2759	91.5	5254	2	BD000706	BD000706	Growth ho
c	17	2759	91.5	5254	2	AR562813	AR562813	Sequence
c	18	2759	91.5	5254	2	AX138941	AX138941	Sequence
c	19	2754.2	91.4	5899	2	AR231272	AR231272	Sequence
c	20	2754.2	91.4	7528	2	AX080953	AX080953	Sequence
c	21	2746.2	91.1	7521	2	AX080951	AX080951	Sequence
c	22	2742.2	91.0	5845	2	AR231271	AR231271	Sequence
c	23	2692.6	89.3	11358	2	BD008820	BD008820	Compositi
c	24	2665.2	88.4	6978	2	AR435506	AR435506	Sequence
c	25	2665.2	88.4	7099	2	AX180761	AX180761	Sequence
c	26	2665.2	88.4	8366	2	AR435498	AR435498	Sequence
c	27	2665.2	88.4	8366	2	AX180752	AX180752	Sequence
c	28	2662.2	88.3	4779	2	AX080955	AX080955	Sequence
c	29	2662.2	88.3	5310	2	AX080989	AX080989	Sequence
c	30	2662.2	88.3	5322	2	AX080956	AX080956	Sequence
c	31	2662.2	88.3	5900	2	AR064320	AR064320	Sequence
c	32	2662.2	88.3	5900	2	BD008816	BD008816	Compositi
c	33	2662.2	88.3	5952	2	AR064321	AR064321	Sequence
c	34	2662.2	88.3	5952	2	BD008817	BD008817	Compositi
c	35	2660.6	88.3	5676	2	AR064322	AR064322	Sequence
c	36	2660.6	88.3	5676	2	BD008818	BD008818	Compositi
c	37	2660.6	88.3	5682	2	AR064323	AR064323	Sequence
c	38	2660.6	88.3	5682	2	BD008819	BD008819	Compositi
c	39	2437.8	80.9	6319	2	CS078974	CS078974	Sequence
c	40	2436.2	80.8	5039	2	CS078949	CS078949	Sequence
c	41	2436.2	80.8	5549	2	AX427842	AX427842	Sequence
c	42	2436.2	80.8	5549	2	AX427843	AX427843	Sequence
c	43	2436.2	80.8	5549	2	AX427844	AX427844	Sequence
c	44	2436.2	80.8	5549	2	AX427845	AX427845	Sequence
c	45	2436.2	80.8	6096	2	CS078963	CS078963	Sequence

ALIGNMENTS

RESULT 1

BD000697/c

LOCUS BD000697 5108 bp DNA linear PAT 31-JAN-2002
 DEFINITION Growth hormone and growth hormone-releasing hormone composition.
 ACCESSION BD000697
 VERSION BD000697.1 GI:18623810
 KEYWORDS JP 2000350590-A/50.
 SOURCE synthetic construct
 ORGANISM synthetic construct

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OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 15:50:12 ; Search time 1122.04 Seconds
(without alignments)
16207.366 Million cell updates/sec

Title: US-10-757-343-2
Perfect score: 9719
Sequence: 1 tggaagggctaattcactcc.....gtggaaaatctctagcaggt 9719

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	9531.2	98.1	9719	3	US-09-700-304-1	Sequence 1, Appli
2	9433.8	97.1	9609	3	US-09-827-688-4	Sequence 4, Appli
3	9206.8	94.7	9709	2	US-08-188-583-5	Sequence 5, Appli
4	9206.8	94.7	9709	3	US-08-388-353-1	Sequence 1, Appli
5	9206.8	94.7	9709	3	US-08-488-551B-1	Sequence 1, Appli
6	9206.8	94.7	9709	3	US-09-309-572-15	Sequence 15, Appl
7	9206.8	94.7	9709	3	US-09-718-096-15	Sequence 15, Appl

8	8724	89.8	8933	3	US-08-463-210-4	Sequence 4, Appli
9	8724	89.8	8933	3	US-09-620-958A-3	Sequence 3, Appli
10	8724	89.8	8933	3	US-08-463-028-4	Sequence 4, Appli
11	8724	89.8	8933	3	US-08-463-209-4	Sequence 4, Appli
12	8724	89.8	8933	3	US-09-943-286-3	Sequence 3, Appli
13	8723	89.8	8932	3	US-09-124-900-1	Sequence 1, Appli
14	8711.2	89.6	8933	3	US-09-620-958A-4	Sequence 4, Appli
15	8711.2	89.6	8933	3	US-09-943-286-4	Sequence 4, Appli
16	8706.4	89.6	8933	3	US-09-620-958A-9	Sequence 9, Appli
17	8706.4	89.6	8933	3	US-09-943-286-9	Sequence 9, Appli
18	8668	89.2	9746	2	US-08-022-835-3	Sequence 3, Appli
19	8668	89.2	9746	2	US-08-388-809-3	Sequence 3, Appli
20	8668	89.2	9746	2	US-08-647-714-3	Sequence 3, Appli
21	8666.4	89.2	9739	2	US-08-022-835-1	Sequence 1, Appli
22	8666.4	89.2	9739	2	US-08-388-809-1	Sequence 1, Appli
23	8666.4	89.2	9739	2	US-08-647-714-1	Sequence 1, Appli
24	8582.8	88.3	9737	2	US-08-944-449-7	Sequence 7, Appli
25	8582.8	88.3	9737	3	US-09-353-362-7	Sequence 7, Appli
26	8582.8	88.3	9737	3	US-09-827-688-12	Sequence 12, Appl
27	8484.4	87.3	15581	3	US-08-646-538-35	Sequence 35, Appl
28	8484.4	87.3	15581	3	US-09-503-222-35	Sequence 35, Appl
29	7616.4	78.4	12494	3	US-08-935-312-13	Sequence 13, Appl
30	7616.4	78.4	12494	3	US-08-848-760B-33	Sequence 33, Appl
31	7611.4	78.3	12479	3	US-09-318-138-13	Sequence 13, Appl
32	7351.4	75.6	9207	3	US-08-388-353-800	Sequence 800, App
33	7351.4	75.6	9207	3	US-08-488-551B-800	Sequence 800, App
34	7299.2	75.1	8954	3	US-09-184-418C-6	Sequence 6, Appli
35	7299.2	75.1	8954	3	US-10-290-579A-6	Sequence 6, Appli
36	7055.6	72.6	9913	3	US-09-827-688-11	Sequence 11, Appl
37	6772.4	69.7	8953	3	US-09-184-418C-3	Sequence 3, Appli
38	6772.4	69.7	8953	3	US-10-290-579A-3	Sequence 3, Appli
39	6719.2	69.1	8992	3	US-09-184-418C-4	Sequence 4, Appli
40	6719.2	69.1	8992	3	US-10-290-579A-4	Sequence 4, Appli
41	6713.8	69.1	8968	3	US-09-184-418C-1	Sequence 1, Appli
42	6713.8	69.1	8968	3	US-10-290-579A-1	Sequence 1, Appli
43	6600	67.9	8972	3	US-09-184-418C-9	Sequence 9, Appli
44	6600	67.9	8972	3	US-10-290-579A-9	Sequence 9, Appli
45	6584.8	67.8	9010	3	US-09-184-418C-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-700-304-1

; Sequence 1, Application US/09700304
; Patent No. 6500623
; GENERAL INFORMATION:
; APPLICANT: GeneCure, LLC
; APPLICANT: Tung, Frank Y.T.
; TITLE OF INVENTION: Replication Defective HIV Vaccine
; FILE REFERENCE: 00714PCTUS
; CURRENT APPLICATION NUMBER: US/09/700,304
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: PCT/US99/10523
; PRIOR FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 60/085,115

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 01:23:04 ; Search time 3629.45 Seconds
(without alignments)
18670.376 Million cell updates/sec

Title: US-10-757-343-2
Perfect score: 9719
Sequence: 1 tggaagggttaattcactcc.....gtggaaaatctctagcaggt 9719

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match		Length	DB ID	Description
		DB	ID			
1	9719	100.0	9719	13	ADQ91504	Adq91504 DNA const
2	9531.2	98.1	9719	11	ADM73881	Adm73881 HIV-1 str

3	9531.2	98.1	9719	12	ADO52557	Ado52557 Human imm
4	9531.2	98.1	9719	14	AEB54637	Aeb54637 HIV-1 (HX
5	9531.2	98.1	9719	14	AED64721	Aed64721 Human imm
6	9518	97.9	9749	2	AAQ45922	Aaq45922 HTLV-III
7	9442.6	97.2	9745	1	AAN60240	Aan60240 HTLV-III
8	9433.8	97.1	9609	6	AAD25515	Aad25515 Human imm
9	9259.6	95.3	9965	6	ABQ81389	Abq81389 HIV-1 R8
10	9210	94.8	9709	12	ADP84804	Adp84804 HIV-1 hyb
11	9208.4	94.7	14824	15	AEE40105	Aee40105 HIV1 NL4-
12	9206.8	94.7	9709	2	AAQ96140	Aaq96140 HIV-1 NL4
13	9206.8	94.7	9709	2	AAV81871	Aav81871 Nucleic a
14	9206.8	94.7	9709	3	AAA40298	Aaa40298 HIV-1 vir
15	9206.8	94.7	9709	3	AAZ88127	Aaz88127 HIV-1 NY5
16	9206.8	94.7	9709	3	AAA97926	Aaa97926 HIV-1 env
17	9206.8	94.7	9709	6	ABQ76897	Abq76897 HIV-1 NL4
18	9206.8	94.7	9709	8	ABS57823	Abs57823 HIV-1 gen
19	9206.8	94.7	9709	12	ADO52559	Ado52559 Human imm
20	9206.8	94.7	9709	14	ADZ26365	Adz26365 HIV-1 com
21	9206.8	94.7	9709	14	ADZ26364	Adz26364 HIV-1 pre
22	9206.8	94.7	9709	15	AEF69293	Aef69293 Human imm
23	9205.2	94.7	9709	14	ADZ26366	Adz26366 HIV-1 com
24	9191	94.6	9709	2	AAQ22488	Aaq22488 HIV-1 pro
25	9014.6	92.8	9425	2	AAQ45919	Aaq45919 HTLV-III
26	9001.2	92.6	9181	5	AAF24377	Aaf24377 Human imm
27	9001.2	92.6	9181	8	AAL53720	Aal53720 HIV-1 DNA
28	9001.2	92.6	9181	8	AAD49652	Aad49652 Human imm
29	9001.2	92.6	9181	12	ADN36409	Adn36409 HIV gene
30	8991	92.5	9213	2	AAV74271	Aav74271 HTLV-III
31	8979.8	92.4	9193	10	ACC70123	Acc70123 Nucleotid
32	8975.4	92.3	9213	2	AAV81866	Aav81866 Nucleic a
33	8975.4	92.3	9213	9	ACD27911	Acd27911 Human lym
34	8975.4	92.3	9213	12	ADO26430	Ado26430 Human T-c
35	8966	92.3	9193	6	AAL49920	Aal49920 Lymphaden
36	8964.2	92.2	9213	1	AAN60288	Aan60288 Sequence
37	8960.6	92.2	9427	2	AAQ45920	Aaq45920 HTLV-III
38	8959.6	92.2	9193	1	AAN60365	Aan60365 Sequence
39	8947.4	92.1	9425	2	AAQ45921	Aaq45921 HTLV-III
40	8940.8	92.0	9229	12	ADO52558	Ado52558 Human imm
41	8940.8	92.0	9229	15	AEE70696	Aee70696 CEM15 rec
42	8878.4	91.4	9103	9	ADA49386	Ada49386 Lymphaden
43	8878.4	91.4	9103	12	ADP81476	Adp81476 Lymphaden
44	8878.4	91.4	9103	14	ADZ71144	Adz71144 HIV-1 com
45	8824.2	90.8	9098	9	ADA49378	Ada49378 Lymphaden

ALIGNMENTS

RESULT 1

ADQ91504

ID ADQ91504 standard; DNA; 9719 BP.

XX

AC ADQ91504;

XX

DT 21-OCT-2004 (first entry)

XX

DE DNA construct LW, useful for HIV infection prevention, treatment.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 01:23:04 ; Search time 1125.55 Seconds
 (without alignments)
 18670.376 Million cell updates/sec

Title: US-10-757-343-3
 Perfect score: 3014
 Sequence: 1 ggcgggccgctctagactag.....ggatccgcgccgctctaga 3014

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_8:*
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 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
	No.	Score	Match Length	DB	ID	
	1	3014	100.0	3014	13 ADQ91505	Adq91505 Plasmid D
c	2	2841.6	94.3	3982	6 ABA91505	Aba91505 Vector pl

c	3	2841.6	94.3	3982	12	ADL71104	Adl71104 pGVL1-EGF
c	4	2837.6	94.1	7002	14	ADZ64591	Adz64591 Expressio
c	5	2837.6	94.1	7802	14	ADZ64590	Adz64590 Expressio
c	6	2824.4	93.7	5742	14	ADZ64587	Adz64587 Expressio
c	7	2817.6	93.5	7940	14	ADZ64589	Adz64589 Expressio
c	8	2817.6	93.5	10769	14	ADZ64586	Adz64586 Expressio
c	9	2782	92.3	7677	10	ACF36695	Acf36695 Plasmid v
c	10	2759	91.5	5108	4	AAC86259	Aac86259 Plasmid G
c	11	2759	91.5	5108	4	AAC86258	Aac86258 Plasmid G
c	12	2759	91.5	5108	6	ABK53269	Abk53269 Growth ho
c	13	2759	91.5	5108	6	ABK53270	Abk53270 Growth ho
c	14	2759	91.5	5111	4	AAC86262	Aac86262 CMV IE pr
c	15	2759	91.5	5111	6	ABK53273	Abk53273 Growth ho
c	16	2759	91.5	5185	4	AAC86254	Aac86254 pGHRH-4 c
c	17	2759	91.5	5185	6	ABK53265	Abk53265 Growth ho
c	18	2759	91.5	5188	4	AAC86266	Aac86266 Plasmid G
c	19	2759	91.5	5188	6	ABK53277	Abk53277 Growth ho
c	20	2759	91.5	5254	4	AAC86267	Aac86267 Plasmid p
c	21	2759	91.5	5254	6	ABK85601	Abk85601 Growth ho
c	22	2754.2	91.4	5899	8	ABS55905	Abs55905 DNA plasm
c	23	2754.2	91.4	7528	4	AAF30316	Aaf30316 Bicistron
c	24	2746.2	91.1	7521	4	AAF30315	Aaf30315 Bicistron
c	25	2742.2	91.0	5845	8	ABS55904	Abs55904 DNA plasm
c	26	2717	90.1	5898	2	AAV00677	Aav00677 DNA plasm
c	27	2703.2	89.7	5843	2	AAV00676	Aav00676 DNA plasm
c	28	2677.4	88.8	4710	15	AEE68486	Aee68486 Plasmid v
c	29	2677.4	88.8	5398	15	AEE68485	Aee68485 Plasmid v
c	30	2677.4	88.8	5913	15	AEE68487	Aee68487 Plasmid v
c	31	2677.4	88.8	7765	15	AEE68505	Aee68505 Plasmid v
c	32	2677.4	88.8	7765	15	AEE68504	Aee68504 Plasmid v
c	33	2666	88.5	5302	13	ADU49659	Adu49659 Nucleotid
c	34	2665.2	88.4	5418	15	AEF63448	Aef63448 Plasmid p
c	35	2665.2	88.4	5444	15	AEF63461	Aef63461 Plasmid p
c	36	2665.2	88.4	5646	15	AEF63446	Aef63446 Plasmid p
c	37	2665.2	88.4	6690	15	AEF63454	Aef63454 Plasmid p
c	38	2665.2	88.4	6705	15	AEF63458	Aef63458 Plasmid C
c	39	2665.2	88.4	6903	15	AEF63456	Aef63456 Plasmid p
c	40	2665.2	88.4	6978	6	AAD38657	Aad38657 CMVkan/R-
c	41	2665.2	88.4	6978	10	ABZ58706	Abz58706 DNA seque
c	42	2665.2	88.4	7099	4	AAH22814	Aah22814 DNA seque
c	43	2665.2	88.4	8366	4	AAH22810	Aah22810 DNA seque
c	44	2665.2	88.4	8366	10	ABZ58698	Abz58698 DNA seque
c	45	2665.2	88.4	8900	15	AEF63450	Aef63450 Plasmid p

ALIGNMENTS

RESULT 1

ADQ91505

ID ADQ91505 standard; DNA; 3014 BP.

XX

AC ADQ91505;

XX

DT 21-OCT-2004 (first entry)

XX

DE Plasmid DNA including kanamycin resistance gene.

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 02:58:50 ; Search time 8536.63 Seconds
(without alignments)
19743.258 Million cell updates/sec

Title: US-10-757-343-3
Perfect score: 3014
Sequence: 1 ggcgggccgctctagactag.....ggatccgcggccgctctaga 3014

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
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2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	901	29.9	905	14	DE097456 Oryzias 1
2	896	29.7	899	14	DE257891 Oryzias 1
3	895	29.7	898	14	DE105125 Oryzias 1

	4	893	29.6	896	14	DE101807	DE101807 Oryzias l
	5	893	29.6	896	14	DE104670	DE104670 Oryzias l
	6	893	29.6	896	14	DE255620	DE255620 Oryzias l
c	7	892	29.6	893	14	DE101806	DE101806 Oryzias l
c	8	890.2	29.5	951	8	CV983341	CV983341 UMC-bof_0
	9	890	29.5	893	14	DE104917	DE104917 Oryzias l
	10	889	29.5	892	14	DE104869	DE104869 Oryzias l
c	11	886.4	29.4	894	9	DN641029	DN641029 UMC-bend_
	12	885	29.4	888	14	DE097133	DE097133 Oryzias l
	13	883	29.3	886	14	DE102263	DE102263 Oryzias l
c	14	882	29.3	883	14	DE097316	DE097316 Oryzias l
c	15	882	29.3	883	14	DE264014	DE264014 Oryzias l
	16	882	29.3	885	14	DE258042	DE258042 Oryzias l
	17	881	29.2	884	14	DE096890	DE096890 Oryzias l
c	18	877.4	29.1	1048	8	CO552396	CO552396 AcLy4_50
	19	877	29.1	880	14	DE256544	DE256544 Oryzias l
c	20	876	29.1	876	14	DE098337	DE098337 Oryzias l
c	21	874	29.0	875	14	DE104916	DE104916 Oryzias l
c	22	873	29.0	873	14	DE257460	DE257460 Oryzias l
	23	873	29.0	876	14	DE097980	DE097980 Oryzias l
	24	872	28.9	875	14	DE097115	DE097115 Oryzias l
	25	872	28.9	875	14	DE097211	DE097211 Oryzias l
	26	870	28.9	873	14	DE104479	DE104479 Oryzias l
	27	870	28.9	873	14	DE265629	DE265629 Oryzias l
	28	868.4	28.8	873	14	DE098619	DE098619 Oryzias l
	29	868	28.8	871	14	DE097113	DE097113 Oryzias l
	30	868	28.8	871	14	DE097317	DE097317 Oryzias l
	31	868	28.8	871	14	DE097534	DE097534 Oryzias l
	32	868	28.8	871	14	DE098058	DE098058 Oryzias l
	33	868	28.8	871	14	DE255532	DE255532 Oryzias l
	34	868	28.8	871	14	DE257461	DE257461 Oryzias l
	35	868	28.8	871	14	DE264015	DE264015 Oryzias l
	36	866.4	28.7	871	14	DE096695	DE096695 Oryzias l
	37	864.8	28.7	879	14	DE098022	DE098022 Oryzias l
c	38	864	28.7	865	14	DE261593	DE261593 Oryzias l
	39	864	28.7	867	14	DE097420	DE097420 Oryzias l
	40	863	28.6	866	14	DE097434	DE097434 Oryzias l
	41	863	28.6	866	14	DE098498	DE098498 Oryzias l
	42	863	28.6	866	14	DE103082	DE103082 Oryzias l
	43	863	28.6	866	14	DE104168	DE104168 Oryzias l
	44	863	28.6	866	14	DE104911	DE104911 Oryzias l
	45	863	28.6	866	14	DE256736	DE256736 Oryzias l

ALIGNMENTS

RESULT 1
DE097456
LOCUS DE097456 905 bp DNA linear GSS 15-SEP-2005
DEFINITION Oryzias latipes DNA, clone: ola1-127I23.R, genomic survey sequence.
ACCESSION DE097456
VERSION DE097456.1 GI:68151055
KEYWORDS GSS.
SOURCE Oryzias latipes (Japanese medaka)
ORGANISM Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;